```
                S
                a
                l
                1
     gtcgtcgACAAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
840  +----------+----------+----------+----------+----------+----------  899
     cagcagcTGTTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC


        S  S  T  K  L  T  H  A  H  R  A  Q  H  L  N  S  W  G  D  R  -
           R  R  Q  N  S  H  M  P  T  V  P  S  T  *  T  P  G  G  T  V  -
           V  V  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  -

     TCAGTCTTCCTCTTCCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
900  +----------+----------+----------+----------+----------+----------  959
     AGTCAGAAGGAGAAGGGGGGGTTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC


        Q  S  S  S  S  P  Q  N  P  R  T  P  S  *  S  P  G  P  L  R  -
           S  L  P  L  P  P  K  T  Q  G  H  P  H  D  L  P  D  P  *  G  -
           S  V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  -

     GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
960  +----------+----------+----------+----------+----------+----------  1019
     CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

        S  H  A  W  W  W  T  *  A  T  K  T  L  R  S  S  S  T  G  T  -
           H  M  R  G  G  G  R  E  P  R  R  P  *  G  Q  V  Q  L  V  R  -
           V  T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  -
```

FIG. 1A

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
1020 +---------+---------+---------+---------+---------+--------- 1079
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

```
   W  T  A  W  R  C  I  M  P  R  Q  S  R  G  R  S  S  T  T  A  -
    G  R  R  G  G  A  *  C  Q  D  K  A  A  G  G  A  V  Q  Q  H  -
   V  D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  -
```

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
1080 +---------+---------+---------+---------+---------+--------- 1139
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

```
   R  T  V  W  S  A  S  S  P  S  C  T  R  T  G  *  M  A  R  S  -
    V  P  C  G  Q  R  P  H  R  P  A  P  G  L  A  E  W  Q  G  V  -
   T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  -
```

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
1140 +---------+---------+---------+---------+---------+--------- 1199
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTTGGTAGAGGTTT

```
   T  S  A  R  S  P  T  K  P  S  Q  P  P  S  R  K  P  S  P  K  -
    Q  V  Q  G  L  Q  Q  S  P  P  S  P  H  R  E  N  H  L  Q  S  -
   Y  K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  -
```

FIG. 1B

```
       GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
  1200 +---------+---------+---------+---------+---------+---------+---------- 1259
       CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC


        P  K  G  S  P  E  N  H  R  C  T  P  C  P  H  P  G  M  S  *  -
          Q  R  A  A  P  R  T  T  G  V  H  P  A  P  I  P  G  *  A  D  -
          A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  -


       ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
  1260 +---------+---------+---------+---------+---------+---------+---------- 1319
       TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG


        P  R  T  R  S  A  *  P  A  W  S  K  A  S  I  P  A  T  S  P  -
          Q  E  P  G  Q  P  D  L  P  G  Q  R  L  L  S  Q  R  H  R  R  -
          T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  -


       GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTTG
  1320 +---------+---------+---------+---------+---------+---------+---------- 1379
       CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACAAC


        W  S  G  R  A  M  G  S  R  R  T  T  T  R  P  R  L  P  C  W  -
          G  V  G  E  Q  W  A  A  G  E  Q  L  Q  D  H  A  S  R  V  G  -
          V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  -
```

FIG. 1C

GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG

1380 +---------+---------+---------+---------+---------+---------- 1439

CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

```
 T  P  T  A  P  S  S  S  T  A  S  S  P  W  T  R  A  G  G  S  -
    L  R  R  L  L  L  P  L  Q  Q  A  H  R  G  Q  E  Q  V  A  A  -
 D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  -
```

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG

1440 +---------+---------+---------+---------+---------+---------- 1499

GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

```
 R  G  T  S  S  H  A  P  *  C  M  R  L  C  T  T  T  T  R  R  -
    G  E  R  L  L  M  L  R  D  A  *  G  S  A  Q  P  L  H  A  E  -
 Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -
```

```
                                        N
                                        o
                                        t
                                        1
```

AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGGCGGCCGCgt c

1500 +---------+---------+---------+---------+----- 1545

TTCTCGGAGAGGGACAGAGGCCCATTTACTCACGCCGCCGGCGcag

```
 R  A  S  P  C  L  R  V  N  E  C  G  G  R  V
    E  P  L  P  V  S  G  *  M  S  A  A  A  A
 K  S  L  S  L  S  P  G  K  *  V  R  R  P  R
```

FIG. 1D